



## SEQUENCE LISTING

1

7A ~~708~~

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Chaplin, Jennifer A.

<120> METHODS FOR PRODUCING ENANTIOMERICALLY PURE  
ALPHA-SUBSTITUTED CARBOXYLIC ACIDS

<130> DIVER1440-2

<140> US 09/751,299  
<141> 2000-12-28

<150> 60/254,414  
<151> 2000-12-07

<150> 60/173,609  
<151> 1999-12-29

<160> 4

<170> PatentIn Ver. 2.1

<210> 1  
<211> 1041  
<212> DNA  
<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Obtained from an  
environmental sample

<220>

<221> CDS  
<222> (1)..(1041)

<400> 1

atg tcg gag ccc atg acg aag tat cgc ggc gcg gtc cag gcc gcg 48  
Met Ser Pro Met Thr Lys Tyr Arg Gly Ala Ala Val Gln Ala Ala  
1 5 10 15

ccg gtg ttc ctc gat ctc gac cgc aca gtc gag aaa gcg atc ggc ctg 96  
Pro Val Phe Leu Asp Leu Asp Arg Thr Val Glu Lys Ala Ile Gly Leu  
20 25 30

atc gag cag gcg gcc aag cag gac gtg cgc ctg atc gca ttc cca gag 144  
Ile Glu Gln Ala Ala Lys Gln Asp Val Arg Leu Ile Ala Phe Pro Glu  
35 40 45

act tgg att ccc ggc tat ccc ttt tgg ata tgg ctg ggc gcg ccg gct 192  
Thr Trp Ile Pro Gly Tyr Pro Phe Trp Ile Trp Leu Gly Ala Pro Ala  
50 55 60

tgg ggc atg cgc ttc gtc cag cgc tat ttc gag aat tcg ctc gtg cgc 240  
Trp Gly Met Arg Phe Val Gln Arg Tyr Phe Glu Asn Ser Leu Val Arg  
65 70 75 80

ggc agc aag cag tgg cag gcc ctg gcg gat gcg gcc cgc cgc cac ggc 288  
Gly Ser Lys Gln Trp Gln Ala Leu Ala Asp Ala Ala Arg Arg His Gly  
85 90 95

atg cat gtc gtg gcc ggc tat agc gag cgc gcg ggc ggc agc ctc tat	336
Met His Val Val Ala Gly Tyr Ser Glu Arg Ala Gly Gly Ser Leu Tyr	
100 105 110	
atg ggc cag gcg atc ttc ggc ccc gat ggc gat ctg atc gcc ggc cgc	384
Met Gly Gln Ala Ile Phe Gly Pro Asp Gly Asp Leu Ile Ala Ala Arg	
115 120 125	
cgc aag ctc aag cct acc cat gcg gag cgc acc gtg ttc ggc gag gga	432
Arg Lys Leu Lys Pro Thr His Ala Glu Arg Thr Val Phe Gly Glu Gly	
130 135 140	
gac ggc agc cat ctc gcg gtg cac gat acc gcc atc ggg cgc ctc ggc	480
Asp Gly Ser His Leu Ala Val His Asp Thr Ala Ile Gly Arg Leu Gly	
145 150 155 160	
gcg ctc tgt tgc tgg gag cac atc cag cca ttg tcg aaa tac gcc atg	528
Ala Leu Cys Cys Trp Glu His Ile Gln Pro Leu Ser Lys Tyr Ala Met	
165 170 175	
tac gcc gcc gac gaa cag gtc cac gtc gcg tcg tgg ccg agc ttc agc	576
Tyr Ala Ala Asp Glu Gln Val His Val Ala Ser Trp Pro Ser Phe Ser	
180 185 190	
ctc tat cgc ggc atg gcc tat gcg ctc gga ccg gag gtc aat acc gcc	624
Leu Tyr Arg Gly Met Ala Tyr Ala Leu Gly Pro Glu Val Asn Thr Ala	
195 200 205	
gca agc cag atc tac gcg gtc gag ggc ggc tgc tac gtg ctg gcg tcg	672
Ala Ser Gln Ile Tyr Ala Val Glu Gly Gly Cys Tyr Val Leu Ala Ser	
210 215 220	
tgc gcg acc gtt tcg ccg gag atg atc aag gta ttg gtg gat acg ccc	720
Cys Ala Thr Val Ser Pro Glu Met Ile Lys Val Leu Val Asp Thr Pro	
225 230 235 240	
gac aag gag atg ttc ctc aag gcc ggc ggt ttt gcc atg att ttc	768
Asp Lys Glu Met Phe Leu Lys Ala Gly Gly Phe Ala Met Ile Phe	
245 250 255	
ggg ccc gac ggc cgc gcc ctg gcc gag ccg ctc ccg gag acc gaa gag	816
Gly Pro Asp Gly Arg Ala Leu Ala Glu Pro Leu Pro Glu Thr Glu Glu	
260 265 270	
gga ctg ctg gtc gat atc gac ctc ggc atg atc gcg ttg gcc aag	864
Gly Leu Leu Val Ala Asp Ile Asp Leu Gly Met Ile Ala Leu Ala Lys	
275 280 285	
gcg gcg gcc gat ccg gcg ggc cac tat tca cgg ccc gac gta acg cgg	912
Ala Ala Ala Asp Pro Ala Gly His Tyr Ser Arg Pro Asp Val Thr Arg	
290 295 300	
ctg ctg ctg gat cga cgt ccg gcc caa cgc gtc gtc acg ctt gat gcc	960
Leu Leu Leu Asp Arg Arg Pro Ala Gln Arg Val Val Thr Leu Asp Ala	
305 310 315 320	
gca ttc gaa ccg caa aac gag gac aag ggc gac ggc ccc gcg ctg cgc	1008
Ala Phe Glu Pro Gln Asn Glu Asp Lys Gly Asp Ala Pro Ala Leu Arg	
325 330 335	

gtg gtg gcg gaa agc gcc gcc gcg cag tag  
 Val Val Ala Glu Ser Ala Ala Ala Ala Gln  
 340 345

1041

<210> 2  
 <211> 346  
 <212> PRT  
 <213> Unknown Organism  
 <223> Description of Unknown Organism: Obtained from an  
 environmental sample

<400> 2  
 Met Ser Glu Pro Met Thr Lys Tyr Arg Gly Ala Ala Val Gln Ala Ala  
 1 5 10 15  
 Pro Val Phe Leu Asp Leu Asp Arg Thr Val Glu Lys Ala Ile Gly Leu  
 20 25 30  
 Ile Glu Gln Ala Ala Lys Gln Asp Val Arg Leu Ile Ala Phe Pro Glu  
 35 40 45  
 Thr Trp Ile Pro Gly Tyr Pro Phe Trp Ile Trp Leu Gly Ala Pro Ala  
 50 55 60  
 Trp Gly Met Arg Phe Val Gln Arg Tyr Phe Glu Asn Ser Leu Val Arg  
 65 70 75 80  
 Gly Ser Lys Gln Trp Gln Ala Leu Ala Asp Ala Ala Arg Arg His Gly  
 85 90 95  
 Met His Val Val Ala Gly Tyr Ser Glu Arg Ala Gly Ser Leu Tyr  
 100 105 110  
 Met Gly Gln Ala Ile Phe Gly Pro Asp Gly Asp Leu Ile Ala Ala Arg  
 115 120 125  
 Arg Lys Leu Lys Pro Thr His Ala Glu Arg Thr Val Phe Gly Glu Gly  
 130 135 140  
 Asp Gly Ser His Leu Ala Val His Asp Thr Ala Ile Gly Arg Leu Gly  
 145 150 155 160  
 Ala Leu Cys Cys Trp Glu His Ile Gln Pro Leu Ser Lys Tyr Ala Met  
 165 170 175  
 Tyr Ala Ala Asp Glu Gln Val His Val Ala Ser Trp Pro Ser Phe Ser  
 180 185 190  
 Leu Tyr Arg Gly Met Ala Tyr Ala Leu Gly Pro Glu Val Asn Thr Ala  
 195 200 205  
 Ala Ser Gln Ile Tyr Ala Val Glu Gly Gly Cys Tyr Val Leu Ala Ser  
 210 215 220  
 Cys Ala Thr Val Ser Pro Glu Met Ile Lys Val Leu Val Asp Thr Pro  
 225 230 235 240  
 Asp Lys Glu Met Phe Leu Lys Ala Gly Gly Phe Ala Met Ile Phe  
 245 250 255  
 Gly Pro Asp Gly Arg Ala Leu Ala Glu Pro Leu Pro Glu Thr Glu Glu  
 260 265 270  
 Gly Leu Leu Val Ala Asp Ile Asp Leu Gly Met Ile Ala Leu Ala Lys  
 275 280 285  
 Ala Ala Ala Asp Pro Ala Gly His Tyr Ser Arg Pro Asp Val Thr Arg  
 290 295 300  
 Leu Leu Leu Asp Arg Arg Pro Ala Gln Arg Val Val Thr Leu Asp Ala  
 305 310 315 320  
 Ala Phe Glu Pro Gln Asn Glu Asp Lys Gly Asp Ala Pro Ala Leu Arg  
 325 330 335  
 Val Val Ala Glu Ser Ala Ala Ala Gln  
 340 345

&lt;210&gt; 3

<211> 1014  
<212> DNA  
<213> Unknown Organism

<220>  
<223> Description of Unknown Organism: Obtained from an environmental sample

<220>  
<221> CDS  
<222> (1)..(1014)

<400> 3		48
atg aaa gaa gct atc aag gtc gcc tgc gtg caa gcc gcc ccg atc tac		
Met Lys Glu Ala Ile Lys Val Ala Cys Val Gln Ala Ala Pro Ile Tyr		
1 5 10 15		
atg gat ttg gag gcg acg gtg gac aaa acc att gag ttg atg gaa gaa		96
Met Asp Leu Glu Ala Thr Val Asp Lys Thr Ile Glu Leu Met Glu Glu		
20 25 30		
gca gca cgt aat aat gct cgt ctg atc gcc ttt ccg gaa act tgg att		144
Ala Ala Arg Asn Asn Ala Arg Leu Ile Ala Phe Pro Glu Thr Trp Ile		
35 40 45		
cca ggc tac cca tgg ttt ctt tgg ctt gac tca cca gca tgg gca atg		192
Pro Gly Tyr Pro Trp Phe Leu Trp Leu Asp Ser Pro Ala Trp Ala Met		
50 55 60		
caa ttt gta cgc caa tac cat gag aac tca ttg gag ttg gat ggc cct		240
Gln Phe Val Arg Gln Tyr His Glu Asn Ser Leu Glu Leu Asp Gly Pro		
65 70 75 80		
caa gct aag cgc att tca gat gca gcc aag cgg ttg gga atc atg gtc		288
Gln Ala Lys Arg Ile Ser Asp Ala Ala Lys Arg Leu Gly Ile Met Val		
85 90 95		
acc ctg ggg atg agt gaa cgg gtc ggt ggc acc ctt tac atc agt cag		336
Thr Leu Gly Met Ser Glu Arg Val Gly Gly Thr Leu Tyr Ile Ser Gln		
100 105 110		
tgg ttc ata ggc gat aat ggt gac acc att ggg gcc cgg cga aag ttg		384
Trp Phe Ile Gly Asp Asn Gly Asp Thr Ile Gly Ala Arg Arg Lys Leu		
115 120 125		
aaa cct act ttt gtt gaa cgt act ttg ttc ggc gaa ggg gat ggt tca		432
Lys Pro Thr Phe Val Glu Arg Thr Leu Phe Gly Glu Gly Asp Gly Ser		
130 135 140		
tcg cta gcg gtt ttc gag acg tct gtt gga agg ctg ggt ggc tta tgc		480
Ser Leu Ala Val Phe Glu Thr Ser Val Gly Arg Leu Gly Gly Leu Cys		
145 150 155 160		
tgt tgg gag cac ctt caa ccg cta aca aaa tac gct ttg tat gca caa		528
Cys Trp Glu His Leu Gln Pro Leu Thr Lys Tyr Ala Leu Tyr Ala Gln		
165 170 175		
aat gaa gag att cat tgt gcg gct tgg ccg agc ttt agc ctt tat cct		576
Asn Glu Glu Ile His Cys Ala Ala Trp Pro Ser Phe Ser Leu Tyr Pro		
180 185 190		

aat gcg gcg aaa gcc ctg ggg cct gat gtc aat gta gcg gcc tct cga	624
Asn Ala Ala Lys Ala Leu Gly Pro Asp Val Asn Val Ala Ala Ser Arg	
195 200 205	
atc tat gcc gtt gaa ggg caa tgc ttc gta cta gcg tcg tgt gcg ctc	672
Ile Tyr Ala Val Glu Gly Gln Cys Phe Val Leu Ala Ser Cys Ala Leu	
210 215 220	
gtt tca caa tcc atg atc gat atg ctt tgt aca gat gac gaa aag cat	720
Val Ser Gln Ser Met Ile Asp Met Leu Cys Thr Asp Asp Glu Lys His	
225 230 235 240	
gcg ttg ctt ctg gct ggt gga cac tca cgt atc ata ggg cct gat	768
Ala Leu Leu Leu Ala Gly Gly His Ser Arg Ile Ile Gly Pro Asp	
245 250 255	
ggt ggt gac ttg gtc gcg cct ctt gcc gaa aat gaa gag ggt att ctc	816
Gly Gly Asp Leu Val Ala Pro Leu Ala Glu Asn Glu Glu Gly Ile Leu	
260 265 270	
tac gca aac ctt gat cct gga gta cgc atc ctt gct aaa atg gcg gca	864
Tyr Ala Asn Leu Asp Pro Gly Val Arg Ile Leu Ala Lys Met Ala Ala	
275 280 285	
gac cct gct ggt cat tat tcc cgt ccc gac att act cgc ttg cta ata	912
Asp Pro Ala Gly His Tyr Ser Arg Pro Asp Ile Thr Arg Leu Leu Ile	
290 295 300	
gat cgc agc cct aaa tta ccg gta gtt gaa att gaa ggt gat ctt cgt	960
Asp Arg Ser Pro Lys Leu Pro Val Val Glu Ile Glu Gly Asp Leu Arg	
305 310 315 320	
cct tac gct ttg ggt aaa gcg tct gag acg ggt gcg caa ctc gaa gaa	1008
Pro Tyr Ala Leu Gly Lys Ala Ser Glu Thr Gly Ala Gln Leu Glu Glu	
325 330 335	
att tga	1014
Ile	

&lt;210&gt; 4

&lt;211&gt; 337

&lt;212&gt; PRT

&lt;213&gt; Unknown Organism

&lt;223&gt; Description of Unknown Organism: Obtained from an environmental sample

&lt;400&gt; 4

Met Lys Glu Ala Ile Lys Val Ala Cys Val Gln Ala Ala Pro Ile Tyr	
1 5 10 15	
Met Asp Leu Glu Ala Thr Val Asp Lys Thr Ile Glu Leu Met Glu Glu	
20 25 30	
Ala Ala Arg Asn Asn Ala Arg Leu Ile Ala Phe Pro Glu Thr Trp Ile	
35 40 45	
Pro Gly Tyr Pro Trp Phe Leu Trp Leu Asp Ser Pro Ala Trp Ala Met	
50 55 60	
Gln Phe Val Arg Gln Tyr His Glu Asn Ser Leu Glu Leu Asp Gly Pro	
65 70 75 80	
Gln Ala Lys Arg Ile Ser Asp Ala Ala Lys Arg Leu Gly Ile Met Val	
85 90 95	
Thr Leu Gly Met Ser Glu Arg Val Gly Gly Thr Leu Tyr Ile Ser Gln	

	100	105	110
Trp Phe Ile Gly Asp Asn Gly Asp Thr Ile Gly Ala Arg Arg Lys Leu			
115	120	125	
Lys Pro Thr Phe Val Glu Arg Thr Leu Phe Gly Glu Gly Asp Gly Ser			
130	135	140	
Ser Leu Ala Val Phe Glu Thr Ser Val Gly Arg Leu Gly Gly Leu Cys			
145	150	155	160
Cys Trp Glu His Leu Gln Pro Leu Thr Lys Tyr Ala Leu Tyr Ala Gln			
165	170	175	
Asn Glu Glu Ile His Cys Ala Ala Trp Pro Ser Phe Ser Leu Tyr Pro			
180	185	190	
Asn Ala Ala Lys Ala Leu Gly Pro Asp Val Asn Val Ala Ala Ser Arg			
195	200	205	
Ile Tyr Ala Val Glu Gly Gln Cys Phe Val Leu Ala Ser Cys Ala Leu			
210	215	220	
Val Ser Gln Ser Met Ile Asp Met Leu Cys Thr Asp Asp Glu Lys His			
225	230	235	240
Ala Leu Leu Leu Ala Gly Gly His Ser Arg Ile Ile Gly Pro Asp			
245	250	255	
Gly Gly Asp Leu Val Ala Pro Leu Ala Glu Asn Glu Glu Gly Ile Leu			
260	265	270	
Tyr Ala Asn Leu Asp Pro Gly Val Arg Ile Leu Ala Lys Met Ala Ala			
275	280	285	
Asp Pro Ala Gly His Tyr Ser Arg Pro Asp Ile Thr Arg Leu Leu Ile			
290	295	300	
Asp Arg Ser Pro Lys Leu Pro Val Val Glu Ile Glu Gly Asp Leu Arg			
305	310	315	320
Pro Tyr Ala Leu Gly Lys Ala Ser Glu Thr Gly Ala Gln Leu Glu Glu			
325	330	335	
Ile			